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CJ  
*[Handwritten signature]*  
<120> METHOD FOR OBTAINING PLANT VARIETIES

<130> A33153-PCT-USA 072667.0128

<140> US 09/529,239  
<141> 2000-10-27

<150> PCT/EP98/06977  
<151> 1998-10-09

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<223> Degenerate oligonucleotides UPMU used to isolate AtMSH3 and  
AtMSH6.

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catttctctt aaacggaggg gattacgaat aaagcaatt 99

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Pro	Lys	Ser	Pro	Thr	His	Glu	Pro	Asn	Pro	Val	Ala	Glu	Ser	Ser	Thr	
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																25
																30
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Pro	Pro	Pro	Lys	Ile	Ser	Ala	Thr	Val	Ser	Phe	Ser	Pro	Ser	Lys	Arg	
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																40
																45
aag	ctt	ctc	tcc	gac	cac	ctc	gcc	gcc	tca	ccc	aaa	aag	cct	aaa		291
Lys	Leu	Leu	Ser	Asp	His	Leu	Ala	Ala	Ser	Pro	Lys	Lys	Pro	Lys		
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ctt	tct	cct	cac	act	caa	aac	cca	gta	ccc	gat	ccc	aat	tta	cac	caa	339
Leu	Ser	Pro	His	Thr	Gln	Asn	Pro	Val	Pro	Asp	Pro	Asn	Leu	His	Gln	
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																75
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Arg	Phe	Leu	Gln	Arg	Phe	Leu	Glu	Pro	Ser	Pro	Glu	Glu	Tyr	Val	Pro	
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																95
gaa	acg	tca	tca	tcg	agg	aaa	tac	aca	cca	ttg	gaa	cag	caa	gtg	gtg	435
Glu	Thr	Ser	Ser	Arg	Lys	Tyr	Thr	Pro	Leu	Glu	Gln	Gln	Gln	Val	Val	
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																105
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gag	cta	aag	agc	aag	tac	cca	gat	gtg	gtt	ttg	atg	gtg	gaa	gtt	ggt	483
Glu	Leu	Lys	Ser	Lys	Tyr	Pro	Asp	Val	Val	Leu	Met	Val	Glu	Val	Gly	
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																120
																125
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Tyr	Lys	Ile	Gly	Val	Val	Lys	Gln	Thr	Glu	Thr	Ala	Ala	Ile	Lys	Ser	
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																185
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cat	ggt	gca	aac	cgg	acc	ggc	cct	ttt	ttc	cgg	gga	ctg	tcg	gct	ttg	723
His	Gly	Ala	Asn	Arg	Thr	Gly	Pro	Phe	Phe	Arg	Gly	Leu	Ser	Ala	Leu	
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																200
																205
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																215
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Gly	Gly	Glu	Glu	Gly	Phe	Gly	Ser	Gln	Ser	Asn	Phe	Leu	Val	Cys	Val	
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																230
																235
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Val	Asp	Glu	Arg	Val	Lys	Ser	Glu	Thr	Leu	Gly	Cys	Gly	Ile	Glu	Met	

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260	265	270	
gaa gtt gtt tat gaa gag ttc aat gat aat ttc atg aga agt gga tta Glu Val Val Tyr Glu Glu Phe Asn Asn Phe Met Arg Ser Gly Leu			963
275	280	285	
gag gct gtg att ttg agc ttg tca cca gct gag ctg ttg ctt ggc cag Glu Ala Val Ile Leu Ser Leu Ser Pro Ala Glu Leu Leu Leu Gly Gln			1011
290	295	300	
cct ctt tca caa caa act gag aag ttt ttg gtg gca cat gct gga cct Pro Leu Ser Gln Gln Thr Glu Lys Phe Leu Val Ala Met Ala Gly Pro			1059
305	310	315	320
acc tca aac gtt cga gtg gaa cgt gcc tca ctg gat tgt ttc agc aat Thr Ser Asn Val Arg Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn			1107
325	330	335	
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340	345	350	
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355	360	365	
gga atg tct tgc ttg aca gtt cat aca att atg aac atg cca cat ctg Gly Met Ser Cys Leu Thr Val His Thr Ile Met Asn Met Pro His Leu			1251
370	375	380	
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385	390	395	400
ttt gaa agg atc ctt tac caa ggg gcc tca ttt cgc tct ttg tca agt Phe Glu Arg Ile Leu Tyr Gln Gly Ala Ser Phe Arg Ser Leu Ser Ser			1347
405	410	415	
aac aca gag atg act ctc tca gcc aat act ctg caa cag ttg gag gtt Asn Thr Glu Met Thr Leu Ser Ala Asn Thr Leu Gln Gln Leu Glu Val			1395
420	425	430	
gtg aaa aat aat tca gat gga tcg gaa tct ggc tcc tta ttc cat aat Val Lys Asn Asn Ser Asp Gly Ser Glu Ser Gly Ser Leu Phe His Asn			1443
435	440	445	
atg aat cac aca ctt aca gta tat gct tcc agg ctt ctt aga cac tgg Met Asn His Thr Leu Thr Val Tyr Gly Ser Arg Leu Leu Arg His Trp			1491
450	455	460	
gtg act cat cct cta tgc gat aga aat ttg ata tct gct cgg ctt gat Val Thr His Pro Leu Cys Asp Arg Asn Leu Ile Ser Ala Arg Leu Asp			1539
465	470	475	480
gct gtt tct gag att tct gct tgc atg gga tct cat agt tct tcc cag Ala Val Ser Glu Ile Ser Ala Cys Met Gly Ser His Ser Ser Gln			1587
485	490	495	

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cct	gag	ttt	tat	ctc	gtg	ctc	tcc	tca	gtc	ttg	aca	gct	atg	tct	aga	1683	
Pro	Glu	Phe	Tyr	Leu	Val	Leu	Ser	Ser	Val	Leu	Thr	Ala	Met	Ser	Arg		
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Ser	Ser	Asp	Ile	Gln	Arg	Gly	Ile	Thr	Arg	Ile	Phe	His	Arg	Thr	Ala		
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Lys	Ala	Thr	Glu	Phe	Ile	Ala	Val	Met	Glu	Ala	Ile	Leu	Leu	Ala	Gly		
545							550				555			560			
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Lys	Gln	Ile	Gln	Arg	Leu	Gly	Ile	Lys	Gln	Asp	Ser	Glu	Met	Arg	Ser		
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Ala	Leu	Asn	Lys	Glu	Ala	Ala	Val	Arg	Gly	Asp	Leu	Leu	Asp	Ile	Leu		
610							615					620					
atc	act	tcc	agc	caa	ttt	cct	gag	ctt	gct	gaa	gct	cgc	caa	gca	2019		
Ile	Thr	Ser	Ser	Asp	Gln	Phe	Pro	Glu	Leu	Ala	Glu	Ala	Arg	Gln	Ala		
625							630				635			640			
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Val	Leu	Val	Ile	Arg	Glu	Lys	Leu	Asp	Ser	Ser	Ile	Ala	Ser	Phe	Arg		
645								650					655				
aag	aag	ctc	gct	att	cga	aat	ttg	gaa	ttt	ctt	caa	gtg	tcg	ggg	atc	2115	
Lys	Lys	Leu	Ala	Ile	Arg	Asn	Leu	Glu	Phe	Leu	Gln	Val	Ser	Gly	Ile		
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aca	cat	ttg	ata	gag	ctg	ccc	gtt	gat	tcc	aag	gtc	cct	atg	aat	tgg	2163	
Thr	His	Leu	Ile	Glu	Leu	Pro	Val	Asp	Ser	Lys	Val	Pro	His	Asn	Trp		
675								680					685				
gtg	aaa	gta	aat	agc	acc	aag	aag	act	att	cga	tat	cat	ccc	cca	gaa	2211	
Val	Lys	Val	Asn	Ser	Thr	Lys	Lys	Thr	Ile	Arg	Tyr	His	Pro	Pro	Glu		
690								695					700				
ata	gta	gct	ggc	ttg	gat	gag	cta	gct	cta	gca	act	gaa	cat	ctt	gcc	2259	
Ile	Val	Ala	Gly	Leu	Asp	Glu	Leu	Ala	Leu	Ala	Thr	Glu	His	Leu	Ala		
705								710					715			720	
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Ile	Val	Asn	Arg	Ala	Ser	Trp	Asp	Ser	Phe	Leu	Lys	Ser	Phe	Ser	Arg		
725									730					735			

tac tac aca gat ttt aag gct gcc gtt caa gct ctt gct gca ctg gac	2355		
Tyr Tyr Thr Asp Phe Lys Ala Ala Val Gln Ala Leu Ala Ala Leu Asp			
740	745	750	
tgt ttg cac tcc ctt tca act cta tct aga aac aac aag tat gtc cgt	2403		
Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg			
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ccc gag ttt gtg gat gac tgt gaa cca gtt gag ata aac ata cag tct	2451		
Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser			
770	775	780	
ggc cgt cat cct gta ctg gag act ata tta caa gat aac ttc gtc cca	2499		
Gly Arg His Pro Val Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro			
785	790	795	800
aat gac aca att ttg cat gca gaa ggg gaa tat tgc caa att atc acc	2547		
Asn Asp Thr Ile Leu His Ala Glu Gly Glu Tyr Cys Gln Ile Ile Thr			
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gga cct aac atg gga gga aag agc tgc tat atc cgt caa gtt gct tta	2595		
Gly Pro Asn Met Gly Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu			
820	825	830	
att tcc ata atg gct cag gtt ggt tcc ttt gta cca gcg tca ttc gcc	2643		
Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala			
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Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp			
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Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Leu Ser Glu Ala			
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900	905	910	
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Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe			
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gtc acg cat tac cct gaa ata gct gag atc agt aac gga ttc cca ggt	2931		
Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly			
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tct gtt ggg aca tac cat gtc tcg tat ctg aca ttg cag aag gat aaa	2979		
Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys			
945	950	955	960
ggc agt tat gat cat gat gat gtg acc tac cta tat aag ctt gtg cgt	3027		
Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg			
965	970	975	
ggt ctt tgc agc agg agc ttt ggt ttt aag gtt gct cag ctt gcc cag	3075		

Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln  
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 995 1000 1005

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 35 40 45

Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys  
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Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln  
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Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro  
 85 90 95

Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val

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Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly  
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Tyr Arg Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val  
130                    135                    140

Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val  
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Pro Thr Phe Arg Leu Asn Phe His Val Arg Arg Leu Val Asn Ala Gly  
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Tyr Lys Ile Gly Val Val Lys Gln Thr Glu Thr Ala Ala Ile Lys Ser  
180                    185                    190

His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu  
195                    200                    205

Tyr Thr Lys Ala Thr Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys  
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Gly Gly Glu Glu Gly Phe Gly Ser Gln Ser Asn Phe Leu Val Cys Val  
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Val Asp Glu Arg Val Lys Ser Glu Thr Leu Gly Cys Gly Ile Glu Met  
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Ser Phe Asp Val Arg Val Gly Val Val Glu Ile Ser Thr Gly  
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Glu Val Val Tyr Glu Glu Phe Asn Asp Asn Phe Met Arg Ser Gly Leu  
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Glu Ala Val Ile Leu Ser Leu Ser Pro Ala Glu Leu Leu Gly Gln  
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Pro Leu Ser Gln Gln Thr Glu Lys Phe Leu Val Ala Met Ala Gly Pro  
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Thr Ser Asn Val Arg Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn  
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Gly Asn Ala Val Asp Glu Val Ile Ser Leu Cys Glu Lys Ile Ser Ala  
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Gly Asn Leu Glu Asp Asp Lys Glu Met Lys Leu Glu Ala Ala Glu Lys  
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Gly Met Ser Cys Leu Thr Val His Thr Ile Met Asn Met Pro His Leu  
370                    375                    380

Thr Val Gln Ala Leu Ala Leu Thr Phe Cys His Leu Lys Gln Phe Gly  
385                    390                    395                    400

Phe Glu Arg Ile Leu Tyr Gln Gly Ala Ser Phe Arg Ser Leu Ser Ser  
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Asn Thr Glu Met Thr Leu Ser Ala Asn Thr Leu Gln Gln Leu Glu Val  
420                    425                    430

Val Lys Asn Asn Ser Asp Gly Ser Glu Ser Gly Ser Leu Phe His Asn  
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Met Asn His Thr Leu Thr Val Tyr Gly Ser Arg Leu Leu Arg His Trp  
450 455 460

Val Thr His Pro Leu Cys Asp Arg Asn Leu Ile Ser Ala Arg Leu Asp  
465 470 475 480

Ala Val Ser Glu Ile Ser Ala Cys Met Gly Ser His Ser Ser Gln  
485 490 495

Leu Ser Ser Glu Leu Val Glu Glu Gly Ser Glu Arg Ala Ile Val Ser  
500 505 510

Pro Glu Phe Tyr Leu Val Leu Ser Ser Val Leu Thr Ala Met Ser Arg  
515 520 525

Ser Ser Asp Ile Gln Arg Gly Ile Thr Arg Ile Phe His Arg Thr Ala  
530 535 540

Lys Ala Thr Glu Phe Ile Ala Val Met Glu Ala Ile Leu Leu Ala Gly  
545 550 555 560

Lys Gln Ile Gln Arg Leu Gly Ile Lys Gln Asp Ser Glu Met Arg Ser  
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Met Gln Ser Ala Thr Val Arg Ser Thr Leu Leu Arg Lys Leu Ile Ser  
580 585 590

Val Ile Ser Ser Pro Val Val Val Asp Asn Ala Gly Lys Leu Leu Ser  
595 600 605

Ala Leu Asn Lys Glu Ala Ala Val Arg Gly Asp Leu Leu Asp Ile Leu  
610 615 620

Ile Thr Ser Ser Asp Gln Phe Pro Glu Leu Ala Glu Ala Arg Gln Ala  
625 630 635 640

Val Leu Val Ile Arg Glu Lys Leu Asp Ser Ser Ile Ala Ser Phe Arg  
645 650 655

Lys Lys Leu Ala Ile Arg Asn Leu Glu Phe Leu Gln Val Ser Gly Ile  
660 665 670

Thr His Leu Ile Glu Leu Pro Val Asp Ser Lys Val Pro His Asn Trp  
675 680 685

Val Lys Val Asn Ser Thr Lys Lys Thr Ile Arg Tyr His Pro Pro Glu  
690 695 700

Ile Val Ala Gly Leu Asp Glu Leu Ala Leu Ala Thr Glu His Leu Ala  
705 710 715 720

Ile Val Asn Arg Ala Ser Trp Asp Ser Phe Leu Lys Ser Phe Ser Arg  
725 730 735

Tyr Tyr Thr Asp Phe Lys Ala Ala Val Gln Ala Leu Ala Leu Asp  
740 745 750

Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg  
755 760 765

Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser  
770 775 780

Gly Arg His Pro Val Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro  
785 790 795 800

Asn Asp Thr Ile Leu His Ala Glu Gly Glu Tyr Cys Gln Ile Ile Thr  
805 810 815

Gly Pro Asn Met Gly Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu  
820 825 830

Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala  
835 840 845

Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp  
850 855 860

Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala  
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Ser His Ile Ile Arg Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp  
885 890 895

Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr  
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Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe  
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Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly  
930 935 940

Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys  
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Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg  
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980 985 990

Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala Lys Leu  
995 1000 1005

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ecotype Columbia

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 Asp Val Pro Gly Pro Glu Thr Pro Gly Met Arg Pro Arg Ala Ser Arg  
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 Pro Val Leu Asp Ser Asn Lys Arg Leu Lys Met Leu Gln Asp Pro Val  
     205                       210                       215  
  
 tgt gga gag aag aaa gaa gta aac gaa gga acc aaa ttt gaa tgg ctt 843  
 Cys Gly Glu Lys Lys Glu Val Asn Glu Gly Thr Lys Phe Glu Trp Leu  
     220                       225                       230  
  
 gag tct tct cga atc agg gat gcc aat aga aga cgt cct gat gat ccc 891  
 Glu Ser Ser Arg Ile Arg Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro  
     235                       240                       245                       250  
  
 ctt tac gat aga aag acc tta cac ata cca cct gat gtt ttc aag aaa 939  
 Leu Tyr Asp Arg Lys Thr Leu His Ile Pro Pro Asp Val Phe Lys Lys  
     255                       260                       265  
  
 atg tct gca tca caa aag caa tat tgg agt gtt aag agt gaa tat atg 987  
 Met Ser Ala Ser Gln Lys Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met  
     270                       275                       280  
  
 gac att gtg ctt ttc ttt aaa gtg ggg aaa ttt tat gag ctg tat gag 1035  
 Asp Ile Val Leu Phe Phe Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu  
     285                       290                       295  
  
 cta gat gcg gaa tta ggt cac aag gag ctt gac tgg aag atg acc atg 1083  
 Leu Asp Ala Glu Leu Gly His Lys Glu Leu Asp Trp Lys Met Thr Met  
     300                       305                       310  
  
 agt ggt gtg gga aaa tgc aga cag gtt atc tct gaa agt ggg ata 1131  
 Ser Gly Val Gly Lys Cys Arg Gln Val Gly Ile Ser Glu Ser Gly Ile  
     315                       320                       325                       330  
  
 gat gag gca gtg caa aag cta tta gct cgt gga tat aaa gtt gga cga 1179  
 Asp Glu Ala Val Gln Lys Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg  
     335                       340                       345

atc gag cag cta gaa aca tct gac caa gca aaa gcc aga ggt gct aat		1227	
Ile Glu Gln Ileu Glu Thr Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn			
350	355	360	
act ata att cca agg aag cta gtt cag gta act cca tca aca gca		1275	
Thr Ile Ile Pro Arg Lys Leu Val Gln Val Leu Thr Pro Ser Thr Ala			
365	370	375	
agc gag gga aac atc ggg cct gat gcc gtc cat ctt ctt gct ata aaa		1323	
Ser Glu Gly Asn Ile Gly Pro Asp Ala Val His Leu Leu Ala Ile Lys			
380	385	390	
gag atc aaa atg gag cta caa aag tgt tca act gtg tat gga ttt gct		1371	
Glu Ile Lys Met Glu Leu Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala			
395	400	405	410
ttt gtt gac tgt gct gcc ttg agg ttt tgg gtt ggg tcc atc agc gat		1419	
Phe Val Asp Cys Ala Ala Leu Arg Phe Trp Val Gly Ser Ile Ser Asp			
415	420	425	
gat gca tca tgt gct gct ctt gga gcg tta ttg atg cag gtt tct cca		1467	
Asp Ala Ser Cys Ala Ala Leu Gly Ala Leu Leu Met Gln Val Ser Pro			
430	435	440	
aag gaa gtg tta tat gac agt aaa ggg cta tca aga gaa gca caa aag		1515	
Lys Glu Val Leu Tyr Asp Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys			
445	450	455	
gct cta agg aaa tat acg ttg aca ggg tct acg gcg gta cag ttg gct		1563	
Ala Leu Arg Lys Tyr Thr Leu Thr Gly Ser Thr Ala Val Gln Leu Ala			
460	465	470	
cca gta cca caa gta atg ggg gat aca gat gct gct gga gtt aga aat		1611	
Pro Val Pro Gln Val Met Gly Asp Thr Asp Ala Ala Gly Val Arg Asn			
475	480	485	490
ata ata gaa tct aac gga tac ttt aaa ggt tct tct gaa tca tgg aac		1659	
Ile Ile Glu Ser Asn Gly Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn			
495	500	505	
tgt gct gtt gat ggt cta aat gaa tgt gat gtt gcc ctt agt gct ctt		1707	
Cys Ala Val Asp Gly Leu Asn Glu Cys Asp Val Ala Leu Ser Ala Leu			
510	515	520	
gga gag cta att aat cat ctg tct agg cta aag cta gaa gat gta ctt		1755	
Gly Glu Leu Ile Asn His Leu Ser Arg Leu Lys Leu Glu Asp Val Leu			
525	530	535	
aag cat ggg gat att ttt cca tac caa gtt tac agg ggt tgt ctc aga		1803	
Lys His Gly Asp Ile Phe Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg			
540	545	550	
att gat ggc cag acg atg gta aat ctt gag ata ttt aac aat agc tgt		1851	
Ile Asp Gly Gln Thr Met Val Asn Leu Glu Ile Phe Asn Asn Ser Cys			
555	560	565	570
gat ggt ggt cct tca ggg acc ttg tac aaa tat ctt gat aac tgt gtt		1899	
Asp Gly Gly Pro Ser Gly Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val			
575	580	585	
agt cca act ggt aag cga ctc tta agg aat tgg atc tgc cat cca ctc		1947	

Ser Pro Thr Gly Lys Arg Leu Leu Arg Asn Trp Ile Cys His Pro Leu  
 590 595 600  
 aaa gat gta gaa agc atc aat aaa cgg ctt gat gta gtt gaa gaa ttc 1995  
 Lys Asp Val Glu Ser Ile Asn Lys Arg Leu Asp Val Val Glu Glu Phe  
 605 610 615  
 acg gca aac tca gaa agt atg caa atc act ggc cag tat ctc cac aaa 2043  
 Thr Ala Asn Ser Glu Ser Met Gln Ile Thr Gly Gln Tyr Leu His Lys  
 620 625 630  
 ctt cca gac tta gaa aga ctg ctc gga cgc atc aag tct agc gtt cga 2091  
 Leu Pro Asp Leu Glu Arg Leu Leu Gly Arg Ile Lys Ser Ser Val Arg  
 635 640 645 650  
 tca tca gcc tct gtg ttg cct gct ctt ctg ggg aaa aaa gtg ctg aaa 2139  
 Ser Ser Ala Ser Val Leu Pro Ala Leu Leu Gly Lys Lys Val Leu Lys  
 655 660 665  
 caa cga gtt aaa gca ttt ggg caa att gtg aaa ggg ttc aga agt gga 2187  
 Gln Arg Val Lys Ala Phe Gly Gln Ile Val Lys Gly Phe Arg Ser Gly  
 670 675 680  
 att gat ctg ttg ttg gct cta cag aag gaa tca aat atg atg agt ttg 2235  
 Ile Asp Leu Leu Ala Leu Gln Lys Glu Ser Asn Met Met Ser Leu  
 685 690 695  
 ctt tat aaa ctc tgt aaa ctt cct ata tta gta gga aaa agc ggg cta 2283  
 Leu Tyr Lys Leu Cys Lys Leu Pro Ile Leu Val Gly Lys Ser Gly Leu  
 700 705 710  
 gag tta ttt ctt tct caa ttc gaa gca gcc ata gat agc gac ttt cca 2331  
 Glu Leu Phe Leu Ser Gln Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro  
 715 720 725 730  
 aat tat cag aac caa gat gtg aca gat gaa aac gct gaa act ctc aca 2379  
 Asn Tyr Gln Asn Gln Asp Val Thr Asp Glu Asn Ala Glu Thr Leu Thr  
 735 740 745  
 ata ctt atc gaa ctt ttt atc gaa aga gca act caa tgg tct gag gtc 2427  
 Ile Leu Ile Glu Leu Phe Ile Glu Arg Ala Thr Gln Trp Ser Glu Val  
 750 755 760  
 att cac acc ata agc tgc cta gat gtc ctg aga tct ttt gca atc gca 2475  
 Ile His Thr Ile Ser Cys Leu Asp Val Leu Arg Ser Phe Ala Ile Ala  
 765 770 775  
 gca agt ctc tct gct gga agc atg gcc agg cct gtt att ttt ccc gaa 2523  
 Ala Ser Leu Ser Ala Gly Ser Met Ala Arg Pro Val Ile Phe Pro Glu  
 780 785 790  
 tca gaa gct aca gat cag aat cag aaa aca aaa ggg cca ata ctt aaa 2571  
 Ser Glu Ala Thr Asp Gln Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys  
 795 800 805 810  
 atc caa gga cta tgg cat cca ttt gca gtt gca gcc gat ggt caa ttg 2619  
 Ile Gln Gly Leu Trp His Pro Phe Ala Val Ala Ala Asp Gly Gln Leu  
 815 820 825  
 cct gtt ccg aat gat ata ctc ctt ggc gag gct aga aga agc agt ggc 2667  
 Pro Val Pro Asn Asp Ile Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly

830	835	840	
agc att cat cct cggttgc tca ctg acggaa cca aac atggc gga			2715
Ser Ile His Pro Arg Ser Leu Leu Leu Thr Gly Pro Asn Met Gly Gly			
845	850	855	
aaa tca act ctt ctt cgt gca aca tgt ctggcc gtt atc ttt gcc caa			2763
Lys Ser Thr Leu Leu Arg Ala Thr Cys Leu Ala Val Ile Phe Ala Gln			
860	865	870	
ctt ggc tgc tac gtg ccgttgt gag tct tgc gaa atc tcc ctc gtg gat			2811
Leu Gly Cys Tyr Val Pro Cys Glu Ser Cys Glu Ile Ser Leu Val Asp			
875	880	885	890
act atc ttc aca agg ctt ggc gca tct gat aga atc atg aca gga gag			2859
Thr Ile Phe Thr Arg Leu Gly Ala Ser Asp Arg Ile Met Thr Gly Glu			
895	900	905	
agt acc ttt ttgtgtactgactgactgactgactgactgactgactgactgactgactg			2907
Ser Thr Phe Leu Val Glu Cys Thr Glu Thr Ala Ser Val Leu Gln Asn			
910	915	920	
gca act cag gat tca cta gta atc ctt gac gaa ctggc aga gga act			2955
Ala Thr Gln Asp Ser Leu Val Ile Leu Asp Glu Leu Gly Arg Gly Thr			
925	930	935	
agt act ttc gat gga tac gcc att gca tac tcgtttcgactcacctg			3003
Ser Thr Phe Asp Gly Tyr Ala Ile Ala Tyr Ser Val Phe Arg His Leu			
940	945	950	
gta gag aaa gtt caa tgt cggtatgc ttt gca aca cat tac cac cct			3051
Val Glu Lys Val Gln Cys Arg Met Leu Phe Ala Thr His Tyr His Pro			
955	960	965	970
ctc acc aag gaa ttc gcgttccacccatgttgcaccatcgaaaacatgt			3099
Leu Thr Lys Glu Phe Ala Ser His Pro Arg Val Thr Ser Lys His Met			
975	980	985	
gct tgc gca ttc aaa tca aga tct gat tat caa cca cgt ggt tgt gat			3147
Ala Cys Ala Phe Lys Ser Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp			
990	995	1000	
caa gac cta gtg ttc ttgtac cgtttaaccgaggaa gcttgtcctgag			3195
Gln Asp Leu Val Phe Leu Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu			
1005	1010	1015	
agc tac gga ctt caa gtg gca ctc atg gct gga ata cca aac caa gtg			3243
Ser Tyr Gly Leu Gln Val Ala Leu Met Ala Gly Ile Pro Asn Gln Val			
1020	1025	1030	
gtt gaa aca gca tca ggt gct gct caa gcc atg aag aga tca att ggg			3291
Val Glu Thr Ala Ser Gly Ala Ala Gln Ala Met Lys Arg Ser Ile Gly			
1035	1040	1045	1050
gga aac ttc aag tca agt gag cta aga tct gag ttc tca agt ctg cat			3339
Glu Asn Phe Lys Ser Ser Glu Leu Arg Ser Glu Phe Ser Ser Leu His			
1055	1060	1065	
gaa gac tgg ctc aag tca ttgtgtggatttctcgatgttgcggcccacaac			3387
Glu Asp Trp Leu Lys Ser Leu Val Gly Ile Ser Arg Val Ala His Asn			
1070	1075	1080	

aat gcc ccc att ggc gaa gat gac tac gac act ttg ttt tgc tta tgg 3435  
Asn Ala Pro Ile Gly Glu Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp  
1085 1090 1095

cat gag atc aaa tcc tct tac tgt gtt ccc aaa taaaatggcta 3478  
His Glu Ile Lys Ser Ser Tyr Cys Val Pro Lys  
1100 1105

tgacataaca ctatctgaag ctcgttaagt ctttgcctc tctgatgttt attcctctta  
3538  
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3598  
aaaaaaaaa 3606

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1 5 10 15

Ala Thr Thr Lys Gly Leu Val Ser Gly Asp Ala Ala Ser Gly Gly  
20 25 30

Gly Ser Gly Gly Pro Arg Phe Asn Val Arg Glu Gly Asp Ala Lys Gly  
35 40 45

Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg  
50 55 60

Gly Thr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser  
65 70 75 80

Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser  
85 90 95

Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly  
100 105 110

Glu Arg Ser Arg Glu Asp Val Val Pro Leu Asn Asp Ser Ser Leu Cys  
115 120 125

Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys  
130 135 140

Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu  
145 150 155 160

Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu  
165 170 175

Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu  
180 185 190

Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn

195                    200                    205

Lys Arg Leu Lys Met Leu Gln Asp Pro Val Cys Gly Glu Lys Lys Glu  
210                    215                    220

Val Asn Glu Gly Thr Lys Phe Glu Trp Leu Glu Ser Ser Arg Ile Arg  
225                    230                    235                    240

Asp Ala Asn Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr  
245                    250                    255

Leu His Ile Pro Pro Asp Val Phe Lys Lys Met Ser Ala Ser Gln Lys  
260                    265                    270

Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe  
275                    280                    285

Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly  
290                    295                    300

His Lys Glu Leu Asp Trp Lys Met Thr Met Ser Gly Val Gly Lys Cys  
305                    310                    315                    320

Arg Gln Val Gly Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys  
325                    330                    335

Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg Ile Glu Gln Leu Glu Thr  
340                    345                    350

Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn Thr Ile Ile Pro Arg Lys  
355                    360                    365

Leu Val Gln Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly  
370                    375                    380

Pro Asp Ala Val His Leu Leu Ala Ile Lys Glu Ile Lys Met Glu Leu  
385                    390                    395                    400

Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala Phe Val Asp Cys Ala Ala  
405                    410                    415

Leu Arg Phe Trp Val Gly Ser Ile Ser Asp Asp Ala Ser Cys Ala Ala  
420                    425                    430

Leu Gly Ala Leu Leu Met Gln Val Ser Pro Lys Glu Val Leu Tyr Asp  
435                    440                    445

Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys Ala Leu Arg Lys Tyr Thr  
450                    455                    460

Leu Thr Gly Ser Thr Ala Val Gln Leu Ala Pro Val Pro Gln Val Met  
465                    470                    475                    480

Gly Asp Thr Asp Ala Ala Gly Val Arg Asn Ile Ile Glu Ser Asn Gly  
485                    490                    495

Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn Cys Ala Val Asp Gly Leu  
500                    505                    510

Asn Glu Cys Asp Val Ala Leu Ser Ala Leu Gly Glu Leu Ile Asn His  
515                    520                    525

Leu Ser Arg Leu Lys Leu Glu Asp Val Leu Lys His Gly Asp Ile Phe  
530 535 540

Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg Ile Asp Gly Gln Thr Met  
545 550 555 560

Val Asn Leu Glu Ile Phe Asn Asn Ser Cys Asp Gly Gly Pro Ser Gly  
565 570 575

Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val Ser Pro Thr Gly Lys Arg  
580 585 590

Leu Leu Arg Asn Trp Ile Cys His Pro Leu Lys Asp Val Glu Ser Ile  
595 600 605

Asn Lys Arg Leu Asp Val Val Glu Glu Phe Thr Ala Asn Ser Glu Ser  
610 615 620

Met Gln Ile Thr Gly Gln Tyr Leu His Lys Leu Pro Asp Leu Glu Arg  
625 630 635 640

Leu Leu Gly Arg Ile Lys Ser Ser Val Arg Ser Ser Ala Ser Val Leu  
645 650 655

Pro Ala Leu Leu Gly Lys Lys Val Leu Lys Gln Arg Val Lys Ala Phe  
660 665 670

Gly Gln Ile Val Lys Gly Phe Arg Ser Gly Ile Asp Leu Leu Leu Ala  
675 680 685

Leu Gln Lys Glu Ser Asn Met Met Ser Leu Leu Tyr Lys Leu Cys Lys  
690 695 700

Leu Pro Ile Leu Val Gly Lys Ser Gly Leu Glu Leu Phe Leu Ser Gln  
705 710 715 720

Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro Asn Tyr Gln Asn Gln Asp  
725 730 735

Val Thr Asp Glu Asn Ala Glu Thr Leu Thr Ile Leu Ile Glu Leu Phe  
740 745 750

Ile Glu Arg Ala Thr Gln Trp Ser Glu Val Ile His Thr Ile Ser Cys  
755 760 765

Leu Asp Val Leu Arg Ser Phe Ala Ile Ala Ala Ser Leu Ser Ala Gly  
770 775 780

Ser Met Ala Arg Pro Val Ile Phe Pro Glu Ser Glu Ala Thr Asp Gln  
785 790 795 800

Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys Ile Gln Gly Leu Trp His  
805 810 815

Pro Phe Ala Val Ala Ala Asp Gly Gln Leu Pro Val Pro Asn Asp Ile  
820 825 830

Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly Ser Ile His Pro Arg Ser  
835 840 845

Leu Leu Leu Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg  
850 855 860

Ala Thr Cys Leu Ala Val Ile Phe Ala Gln Leu Gly Cys Tyr Val Pro  
865 870 875 880

Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu  
885 890 895

Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu  
900 905 910

Cys Thr Glu Thr Ala Ser Val Leu Gln Asn Ala Thr Gln Asp Ser Leu  
915 920 925

Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr Phe Asp Gly Tyr  
930 935 940

Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys  
945 950 955 960

Arg Met Leu Phe Ala Thr His Tyr His Pro Leu Thr Lys Glu Phe Ala  
965 970 975

Ser His Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser  
980 985 990

Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp Gln Asp Leu Val Phe Leu  
995 1000 1005

Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu Ser Tyr Gly Leu Gln Val  
1010 1015 1020

Ala Leu Met Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala Ser Gly  
1025 1030 1035 1040

Ala Ala Gln Ala Met Lys Arg Ser Ile Gly Glu Asn Phe Lys Ser Ser  
1045 1050 1055

Glu Leu Arg Ser Glu Phe Ser Ser Leu His Glu Asp Trp Leu Lys Ser  
1060 1065 1070

Leu Val Gly Ile Ser Arg Val Ala His Asn Asn Ala Pro Ile Gly Glu  
1075 1080 1085

Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp His Glu Ile Lys Ser Ser  
1090 1095 1100

Tyr Cys Val Pro Lys  
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<210> 32  
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<220>  
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microsatellite

<400> 32  
accatgcata gcttaaaactt cttg 24

<210> 33  
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<212> DNA  
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<220>  
<223> Reverse primer for PCR amplification of ATHGENEA microsatellite

<400> 33  
acataaccac aaataggggt gc 22

<210> 34  
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<220>  
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<400> 34  
gaagcgatat tgttcgtg 18

<210> 35  
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<220>  
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<400> 35  
agattgcgag aacattcc 18

<210> 36  
<211> 31  
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<220>  
<223> Forward primer DMCIN-1 for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 36

acgcgtcgac tcagctatga gattactcgt g 31

<210> 37  
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<220>  
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ssp. *Landsberg erecta "Ler"*

<400> 37

gctctagatt tctcgctcta agactctct 29

<210> 38  
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<220>  
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ssp. *Landsberg erecta "Ler"*

<400> 38

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<210> 39  
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<220>  
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ssp. *Landsberg erecta "Ler"*

<400> 39

tccccccgggc tcgagagatc tccatggttt cttagctct atgaatcc 48

<210> 40  
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<220>  
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*Landsberg erecta "Ler"*

<400> 40

acgcgtcgac gaattcgcaa gtgggg 26

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<220>  
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*Landsberg erecta* "Ler"

<400> 41

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<220>  
<223> Forward primer for PCR amplification of ATEAT1 SSLP marker in *Arabidopsis thaliana* subspecies

<400> 42

gccactgcgt gaatgatatg 20

<210> 43  
<211> 22  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Reverse primer for PCR amplification of ATEAT1 SSLP marker in *Arabidopsis thaliana* subspecies

<400> 43

cgaacagcca acattaattc cc 22

<210> 44  
<211> 18  
<212> DNA  
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<220>  
<223> Forward primer for PCR amplification of NGA63 SSLP marker in *Arabidopsis thaliana* subspecies

<400> 44

aaccaaggca cagaagcg 18

<210> 45

<211> 18  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Reverse primer for PCR amplification of NGA63 SSLP marker in  
Arabidopsis  
thaliana subspecies

<400> 45  
  
acccaagtga tcgccacc 18

<210> 46  
<211> 21  
<212> DNA  
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<220>  
<223> Forward primer for PCR amplification of NGA248 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 46  
  
taccgaacca aaacacaaag g 21

<210> 47  
<211> 22  
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<220>  
<223> Reverse primer for PCR amplification of NGA248 SSLP marker in  
Arabidopsis thaliana subspecies

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tctgtatctc ggtgaattct cc 22

<210> 48  
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<220>  
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Arabidopsis thaliana subspecies

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ggtctgttga tgtcgtaagt cg 22

<210> 49  
<211> 22  
<212> DNA  
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<220>  
<223> Reverse primer for PCR amplification of NGA128 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 49

atcttgaaac cttagggag gg 22

<210> 50  
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<212> DNA  
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<220>  
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Arabidopsis thaliana subspecies

<400> 50

ctgatctcac ggacaatagt gc 22

<210> 51  
<211> 20  
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<220>  
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Arabidopsis thaliana subspecies

<400> 51

ggctccataa aaagtgcacc 20

<210> 52  
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<220>  
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Arabidopsis thaliana subspecies

<400> 52

ctccagttgg aagctaaagg g 21

<210> 53  
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<220>  
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Arabidopsis thaliana subspecies

<400> 53

tgttttttag gacaaatggc g 21

<210> 54  
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<212> DNA  
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<220>  
<223> Forward primer for PCR amplification of NGA168 SSLP marker in Arabidopsis thaliana subspecies

<400> 54

ccttcacatc caaaacccac 20

<210> 55  
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<400> 55

gcacataccc acaaccagaa 20

<210> 56  
<211> 20  
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<220>  
<223> Forward primer for PCR amplification of NGA1126 SSLP marker in Arabidopsis thaliana subspecies

<400> 56

cgctacgctt ttccggtaaaag 20

<210> 57  
<211> 20  
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<220>  
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<400> 57

gcacagtcca agtcacacaacc 20

<210> 58

<211> 20  
<212> DNA  
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<220>  
<223> Forward primer for PCR amplification of NGA361 SSLP marker in Arabidopsis thaliana subspecies

<400> 58

aaagagatga gaatttggac 20

<210> 59  
<211> 23  
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acatatcaat atattaaagt agc 23

<210> 60  
<211> 18  
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<220>  
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<400> 60

tcgtctactg cactgccg 18

<210> 61  
<211> 22  
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<220>  
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<400> 61

gaggacatgt ataggagcct cg 22

<210> 62  
<211> 20  
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<223> Forward primer for PCR amplification of AthBIO2 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 62

tgacctccctc ttccatggag 20

<210> 63

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for PCR amplification of AthBIO2 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 63

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<210> 64

<211> 21

<212> DNA

<213> Artificial sequence

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<223> Forward primer for PCR amplification of AthUBIQUE SSLP marker  
in  
Arabidopsis thaliana subspecies

<400> 64

aggcaaatgt ccatttcatt g 21

<210> 65

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for PCR amplification of AthUBIQUE SSLP marker  
in  
Arabidopsis thaliana subspecies

<400> 65

acgacatggc agatttctcc 20

<210> 66

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer for PCR amplification of NGA172 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 66  
agctgcttcc ttatagcgtc c 21

<210> 67  
<211> 19  
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<223> Reverse primer for PCR amplification of NGA172 SSLP marker in Arabidopsis thaliana subspecies

<400> 67  
catccgaatg ccattgttc 19

<210> 68  
<211> 21  
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<220>  
<223> Forward primer for PCR amplification of NGA126 SSLP marker in Arabidopsis thaliana subspecies

<400> 68  
aaaaaaaacgc tactttcgtg g 21

<210> 69  
<211> 22  
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<220>  
<223> Reverse primer for PCR amplification of NGA126 SSLP marker in Arabidopsis thaliana subspecies

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caagagcaat atcaagagca gc 22

<210> 70  
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<220>  
<223> Forward primer for PCR amplification of NGA162 SSLP marker in Arabidopsis thaliana subspecies

<400> 70  
catgcaattt gcatctgagg 20

<210> 71  
<211> 22  
<212> DNA  
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<220>  
<223> Reverse primer for PCR amplification of NGA162 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 71  
  
ctctgtcaact cttttcctct gg 22

<210> 72  
<211> 21  
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<220>  
<223> Forward primer for PCR amplification of NGA6 SSLP marker in  
Arabidopsis  
thaliana subspecies

<400> 72  
  
tggatttctt cctctcttca c 21

<210> 73  
<211> 21  
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Arabidopsis  
thaliana subspecies

<400> 73  
  
atggagaagc ttacactgat c 21

<210> 74  
<211> 20  
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Arabidopsis  
thaliana subspecies

<400> 74  
  
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<210> 75  
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<212> DNA  
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Arabidopsis  
thaliana subspecies

<400> 75

tgatgctctc tgaaacaaga gc 22

<210> 76  
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<223> Forward primer for PCR amplification of NGA8 SSLP marker in  
Arabidopsis  
thaliana subspecies

<400> 76

gagggcaaata ctttatattcg g 21

<210> 77  
<211> 22  
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Arabidopsis  
thaliana subspecies

<400> 77

tggctttcgt ttataaacat cc 22

<210> 78  
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<223> Forward primer for PCR amplification of NGA1107 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 78

gcgaaaaaac aaaaaaatcc a 21

<210> 79  
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<223> Reverse primer for PCR amplification of NGA1107 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 79

cgacgaatcg acagaattag g 21

<210> 80  
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Arabidopsis thaliana subspecies

<400> 80

gaaatccaaa tcccagagag g 21

<210> 81  
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Arabidopsis thaliana subspecies

<400> 81

tctccccact agttttgtgt cc 22

<210> 82  
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Arabidopsis thaliana subspecies

<400> 82

taccgtcaat ttcatcgcc 19

<210> 83  
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Arabidopsis thaliana subspecies

<400> 83  
ggatccctaa ctgtaaaatc cc 22

<210> 84  
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<223> Forward primer for PCR amplification of CA72 SSLP marker in  
Arabidopsis  
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<400> 84  
aatccagta accaaacaca ca 22

<210> 85  
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<400> 85  
cccagtctaa ccacgaccac 20

<210> 86  
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Arabidopsis thaliana subspecies

<400> 86  
gttttggaa gtttgctgg 20

<210> 87  
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Arabidopsis thaliana subspecies

<400> 87  
cagtctaaaa gcgagagtat gatg 24

<210> 88  
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<400> 88

gttatggagt ttcttagggca cg 22

<210> 89  
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<400> 89

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<210> 90  
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<223> Forward primer for PCR amplification of NGA139 SSLP marker in Arabidopsis thaliana subspecies

<400> 90

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<210> 91  
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<400> 91

ggtttcgttt cactatccag g 21

<210> 92  
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<223> Forward primer for PCR amplification of NGA76 SSLP marker in  
Arabidopsis  
thaliana subspecies

<400> 92

ggagaaaaatg tcactctcca cc 22

<210> 93

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for PCR amplification of NGA76 SSLP marker in  
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thaliana subspecies

<400> 93

aggcatggga gacatttacg 20

<210> 94

<211> 20

<212> DNA

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<223> Forward primer for PCR amplification of ATHSO191 SSLP marker  
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Arabidopsis thaliana subspecies

<400> 94

ctcccaccaat catgcaaatg 20

<210> 95

<211> 21

<212> DNA

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<223> Reverse primer for PCR amplification of ATHSO191 SSLP marker  
in  
Arabidopsis thaliana subspecies

<400> 95

tgatgttgat ggagatggtc a 21

<210> 96

<211> 22

<212> DNA

<213> Artificial sequence

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<223> Forward primer for PCR amplification of NGA129 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 96

tcaggaggaa ctaaagttag gg 22

<210> 97  
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<223> Reverse primer for PCR amplification of NGA129 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 97

cacactgaag atggcttga gg 22

<210> 98  
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<220>  
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<400> 98

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8040 ccccaaactt caagcaacac aa